



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 99611

TO: Jane Zara
Location: CM1/11D03/11E12
Art Unit: 1635
Monday, August 25, 2003
Case Serial Number: 09/590968

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Zara,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2003, 03:19:36 ; Search time 13751 Seconds
(without alignments)
4549.038 Million cell updates/sec

Title: US-09-590-968-2
Perfect score: 9896
Sequence: 1 MWDEPREATIKPSYWLDA.....KRAKDSAAVLELLNKTF 1909

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame-p2n.model -DEV=xl
-O=/cgn2_1/USPTO_spool_p/US09590968/runat_20082003_160724_10527/app_query.fasta_1.2055
-DB=Pending_Patents_NA_Main -QFWT=fastap -SUFFIX=p2n.rnnp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cd1 -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09590968 -CGN_1_1_8611 -runat_20082003_160724_10527
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_Main:
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US080_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US081_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US082_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US083_COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US084_COMB.seq.*
10: /cgn2_6/ptodata/2/pna/US085_COMB.seq.*
11: /cgn2_6/ptodata/2/pna/US086_COMB.seq.*
12: /cgn2_6/ptodata/2/pna/US087_COMB.seq.*
13: /cgn2_6/ptodata/2/pna/US088_COMB.seq.*
14: /cgn2_6/ptodata/2/pna/US089_COMB.seq.*
15: /cgn2_6/ptodata/2/pna/US090_COMB.seq.*
16: /cgn2_6/ptodata/2/pna/US091_COMB.seq.*
17: /cgn2_6/ptodata/2/pna/US092A_COMB.seq.*
18: /cgn2_6/ptodata/2/pna/US092B_COMB.seq.*
19: /cgn2_6/ptodata/2/pna/US093A_COMB.seq.*
20: /cgn2_6/ptodata/2/pna/US093B_COMB.seq.*
21: /cgn2_6/ptodata/2/pna/US094_COMB.seq.*
22: /cgn2_6/ptodata/2/pna/US095A_COMB.seq.*
23: /cgn2_6/ptodata/2/pna/US095B_COMB.seq.*
24: /cgn2_6/ptodata/2/pna/US095C_COMB.seq.*
25: /cgn2_6/ptodata/2/pna/US095D_COMB.seq.*
26: /cgn2_6/ptodata/2/pna/US096A_COMB.seq.*
27: /cgn2_6/ptodata/2/pna/US096B_COMB.seq.*
28: /cgn2_6/ptodata/2/pna/US096C_COMB.seq.*

29: /cgn2_6/ptodata/2/pna/US096D_COMB.seq.*
30: /cgn2_6/ptodata/2/pna/US096E_COMB.seq.*
31: /cgn2_6/ptodata/2/pna/US097A_COMB.seq.*
32: /cgn2_6/ptodata/2/pna/US097B_COMB.seq.*
33: /cgn2_6/ptodata/2/pna/US097C_COMB.seq.*
34: /cgn2_6/ptodata/2/pna/US098A_COMB.seq.*
35: /cgn2_6/ptodata/2/pna/US098B_COMB.seq.*
36: /cgn2_6/ptodata/2/pna/US098C_COMB.seq.*
37: /cgn2_6/ptodata/2/pna/US098D_COMB.seq.*
38: /cgn2_6/ptodata/2/pna/US099A_COMB.seq.*
39: /cgn2_6/ptodata/2/pna/US099B_COMB.seq.*
40: /cgn2_6/ptodata/2/pna/US099C_COMB.seq.*
41: /cgn2_6/ptodata/2/pna/US099D_COMB.seq.*
42: /cgn2_6/ptodata/2/pna/US099E_COMB.seq.*
43: /cgn2_6/ptodata/2/pna/US099F_COMB.seq.*
44: /cgn2_6/ptodata/2/pna/US100A_COMB.seq.*
45: /cgn2_6/ptodata/2/pna/US100B_COMB.seq.*
46: /cgn2_6/ptodata/2/pna/US101A_COMB.seq.*
47: /cgn2_6/ptodata/2/pna/US101B_COMB.seq.*
48: /cgn2_6/ptodata/2/pna/US102A_COMB.seq.*
49: /cgn2_6/ptodata/2/pna/US102B_COMB.seq.*
50: /cgn2_6/ptodata/2/pna/US103A_COMB.seq.*
51: /cgn2_6/ptodata/2/pna/US103B_COMB.seq.*
52: /cgn2_6/ptodata/2/pna/US104A_COMB.seq.*
53: /cgn2_6/ptodata/2/pna/US104B_COMB.seq.*
54: /cgn2_6/ptodata/2/pna/US6000_COMB.seq.*
55: /cgn2_6/ptodata/2/pna/US6001_COMB.seq.*
56: /cgn2_6/ptodata/2/pna/US6002_COMB.seq.*
57: /cgn2_6/ptodata/2/pna/US6003_COMB.seq.*
58: /cgn2_6/ptodata/2/pna/US6004_COMB.seq.*
59: /cgn2_6/ptodata/2/pna/US6005_COMB.seq.*
60: /cgn2_6/ptodata/2/pna/US6006_COMB.seq.*
61: /cgn2_6/ptodata/2/pna/US6007_COMB.seq.*
62: /cgn2_6/ptodata/2/pna/US6008_COMB.seq.*
63: /cgn2_6/ptodata/2/pna/US6009_COMB.seq.*
64: /cgn2_6/ptodata/2/pna/US6010_COMB.seq.*
65: /cgn2_6/ptodata/2/pna/US6011_COMB.seq.*
66: /cgn2_6/ptodata/2/pna/US6012_COMB.seq.*
67: /cgn2_6/ptodata/2/pna/US6013_COMB.seq.*
68: /cgn2_6/ptodata/2/pna/US6014_COMB.seq.*
69: /cgn2_6/ptodata/2/pna/US6015_COMB.seq.*
70: /cgn2_6/ptodata/2/pna/US6016_COMB.seq.*
71: /cgn2_6/ptodata/2/pna/US6017_COMB.seq.*
72: /cgn2_6/ptodata/2/pna/US6018_COMB.seq.*
73: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
74: /cgn2_6/ptodata/2/pna/US6020_COMB.seq.*
75: /cgn2_6/ptodata/2/pna/US6021_COMB.seq.*
76: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
77: /cgn2_6/ptodata/2/pna/US6023A_COMB.seq.*
78: /cgn2_6/ptodata/2/pna/US6023B_COMB.seq.*
79: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
80: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
81: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
82: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
83: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
84: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
85: /cgn2_6/ptodata/2/pna/US6030_COMB.seq.*
86: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
87: /cgn2_6/ptodata/2/pna/US6032_COMB.seq.*
88: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
89: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
90: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
91: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*
92: /cgn2_6/ptodata/2/pna/US6037_COMB.seq.*
93: /cgn2_6/ptodata/2/pna/US6038_COMB.seq.*
94: /cgn2_6/ptodata/2/pna/US6039_COMB.seq.*
95: /cgn2_6/ptodata/2/pna/US6040_COMB.seq.*
96: /cgn2_6/ptodata/2/pna/US6041_COMB.seq.*
97: /cgn2_6/ptodata/2/pna/US6042_COMB.seq.*
98: /cgn2_6/ptodata/2/pna/US6043_COMB.seq.*
99: /cgn2_6/ptodata/2/pna/US6044_COMB.seq.*
100: /cgn2_6/ptodata/2/pna/US6045_COMB.seq.*
101: /cgn2_6/ptodata/2/pna/US6046_COMB.seq.*

Mon Aug 25 09:14:58 2003

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2003, 03:36:41 ; Search time 665 Seconds
(without alignments)
2174.425 Million cell updates/sec

Title: US-09-590-968-2
Perfect score: 9896
Sequence: 1 MVNDEPREATIKPSYWLDA.....KKAKDSAAVLLLELLNKTFS 1909

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 767147 seqs, 378730432 residues

Total number of hits satisfying chosen parameters: 1534294

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL-frame+ p2n.model -DEV-xlp
-O-/cgn2_1/USPTO_spool_p/US09590968/runat_20082003_160724_10551/app_query_fasta_1.2055
-DB-Pending_Patents_NA_New -SUFFIX-p2n.rnpn -MINMATCH-0.1
-LOOPCT-0 -LOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US09590968 @CGN1.1.531 @runat_20082003_160724_10551
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database : Pending Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES